us-09-887-784-4.rspt

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June 3, 2003, 15:02:13; Search time 83 Seconds
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1274-8 USKGEELFTGVVPILVELD......VLLGFVTRAGITIGNDELXK 239
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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sp_virus:*
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SPTREMBL_21:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Q93125 aequorea vi	027903 unidentifie	0961q1 homo sapien		Q17106 aequorea vi	Q8wtc6 aequorea ma	Q8wp95 aequorea ma	O8wtc4 aequorea ma	O8wtd0 aequorea ma	Q8wtc9 aequorea ma	Q8wtc8 aequorea ma	Q8wtc7 aequorea ma	Q8wtc5 aequorea ma	Q95ua7 montastraea	Q963f5 montastraea	Q8t6u0 dendronepht
SUMMARIES	А	093125	027903	096501	017105	017106	QBWTC6	Q8WP95	OSWTC4	QBWTD0	Q8WTC9	OBWIC8	Q8WTC7	Q8WTC5	Q95UA7	Q963F5	Q816U0
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d	Query Match	97.3	97.3	96.3	94.6	93.4	85.2	84.9	84.5	84.4	84.3	84.3	84.1	84.0	19.8	19.4	19.2
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7 1 25 093125	01-FEB-1997 01-FEB-1997	01-JUN-2002	Green fluorescent protein mutant GFP.	Aequorea victoria (Jellyfish).	Eukaryota; Metazoa; Cnidaria;	Aequoreidae; Aequorea. NCBI TaxID-6100:	[1]	SEQUENCE FROM N.A.	MEDLINE-96305137; PubMed-8707053;	Cormack B.P.	"FACS-optimized mutants of the green fluorescent protei	Gene 173:33-	[5]	SEQUENCE FROM N.A.	Cormack B.P.,	Brown A.J.P.;	"Yeast Enhanced Green Fluorescent	expression in Candida	Microbiology	EMBL; U73901	HSSP; P42212; 1	InterPro; IF	Pfam; PF0135	PRINTS; PR01	ProDom; PD013756; Green_fl_protein; 1.	SEQUENCE 2
RESULT 093125 ID Q			OE GN	SO	88	38	R	RP	X.	RA	RŢ	RL	RN	RP	æ	RA	RT	F					DR	DR	DR	ÖS

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in (GPP).";

"Yeast Enhanced Green Fluorescent Protein (yEGPP): a reporter of gene expression in Candida allicans.";

Microbios.ogo (0.00 (1985). 1.

EMBI. 073901. AAB18957.1:
HESP: P4212.1 BEP.

InterPro. IMPROPRIEG Green_fl_protein,

PRINTYS: PRO1229; GFLUORESCENT

PRINTYS: PRO1229; Green_fl_protein, 1.

SEQUENCE 2.38 AAA; 26840 PMF; A26622809949DEA60 CRC64; (2dre 17.33-30(1990). (2dre 17.33-30(1990). SEQUENCE FROM N.A. GOTMACK B.P., Bertram G., Egerton M., Gow N.A.R., Falkow S., Brown A.J.P.;

0; Gaps Query Match 97.3%; Score 1240; DB 5; Length 238; Paet Local Similarity 97.5%; Pred. No. 1.3e-94. Wetches 232; Conservative 2; Mismarches 4; Indels Watches 232; Conservative 2.

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122 NRIELKGIDFKEDGNILGHKLEYNYNSHNYSIMADKQKNGIKVNFKIRHNIEDGSVQLAD 181
                                                                                                                                  VTTLSYGVOCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 121
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2 VSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Received 1 (273.7), Mendes 0., Wolbert E.J.H., de Boer A.D.;
Enhanced expression in tobecco of the gene encoding green fluorescent
protect by modification of its codo usage.,
plant Mol. Biol. 31999-999 (1997).
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01-NOV-1996 (TrEMBIrel. 01, Last sequence update)
01-NOV-2002 (TrEMBIrel. 31, Last annotation update)
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61 LVTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTL 120
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Homo sapiens (Human).
Bukaryota: Wetazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Rutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TAXID-9606;
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Bokaryota: Metazoa: Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae: Aequorea.
WCBL_TRAID-6100;
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Submitted (GNY-1995) to the EMBL/GenBank/DDBJ databases
EMBL 78395; CAMS0799.1;
EMBL 78395; CAMS0796; Green_fl_protein.
Incerpror, IPR00706; Green_fl_protein.
PRINTS; PR01259; GPLUORRSGENT.
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01.NOV-1996 (TrEMBLED: 0). Last sequence update)
01.NOV-1096 (TrEMBLED: 21. Last senotation update)
Green fluorescent protein (Fragment).
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PHELL ABOIRES. BASS (801).

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INEEPTON INFOOTON
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                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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NRIELKGIDEREDGNILGHKLEYNYNSHNYIMADKQKNGIKVNFKIRHNIEDGSVQLAD 181
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LUG W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Qin Y.X., Pang S.O.,
Lug W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Qin Y.X., Pang S.O.,
Lug W.X., Xia N.S.;
Submitted (NVV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, YQ11821, ARX02062.1;
EMBL, AYQ11821, ARX02062.1;
EMBL, RYQ11821, ARX02062.1;
Prob. Prob. PROBOT SEQUENCE CONTROL FROM PROBOT SECUENCE CONTROL PROBOT SEQUENCE CONTROL PROBOT SECUENCE CONTROL SECUENCE CON
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Lio W.X., Zhang J., Yang H.J., Xie X.Y., Ld·S.W., Guan B.Q., Chen M.,
Li S.J., Xia N.S.;
*Colorful mutants of green fluorescent protein from Aequorea
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berna.
Rikaryota; Metazoa; Chidaria; Hydrozoa; Hydroida; Leptomedusae;
Rikaryota; Metazoa; Chidaria; Hydrozoa; Hydroida; Leptomedusae;
                                                                                                                                      Aequorea macrodactyla.
Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85.2%; Score 1085; DB 5; Length 2
82.4%; Pred. No. 7.9e-82;
Live 20; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                          macrodactyla., v. Submitted (CCT-2001) to the EMBL/GenBank/DDBJ databases. EMBL: A4438431; A443316.1; Theterror IRMO(0786; Green_fl_protein. Proposition pro1935; GFP. I protein. Proposition; pro1935; GFP. I protein. Proposition 238 AA: Z7015 MM; GBPPPJSE88926903 CRC64;
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Last annotation update)
                01-MAR-2002 (TERMBLrel. 20, Created)
MAR-2002 (TERMBLrel. 20, Last sequence update)
01-JUN-2002 (TERMBLrel. 21, Last annotation update)
Green floorescent protein.
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Matches 196; Conservative
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Aequoreidae; Aequorea.
NCBI_TaxID=147615;
                                                                                                                                                                                 Aequoreidae; Aequorea.
NCBI_TaxID-147615;
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Best Local Similarity
                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aequorea victoria (Jellyflah).
Eukaryota: Metazoa, Chidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae, Aequorea.
WCBLTAXID-6100;
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                                           Length 238;
                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Warkins J.N., Campbell A.K.;
Submitted (JAW-1995) to the EMBL/GenBank/DDBJ databases.
BEMEL, K83960; CAAS990.1;
BESP; P42212; BIPP.
HISP: P62212; BIPP.
Pf. Carrier Propose (Green_fl_protein.)
Pf. Carrier Propose (Green_fl_protein.)
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26950 MW; 26E2BE450E748E44 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UNY-2002 (TrEMBLrel. 21, Last annotation update)
Green fluorescent protein (Fragment).
                                           94.6%; Score 1205; DB 5;
94.1%; Pred. No. 9.8e-92;
ive 6; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       238 AA
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ProDom; PD013756; Green_fl_protein; 1.
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                                                                                             Matches 224; Conservative
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   238 AA;
                                                                      Similarity
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      SECUENCE
                                                  Query Match
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                                                                      Best Local
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01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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182 HYDONTPICDGSVILPDNHYLSTOSALSKDPNEKRDHWYLLGFVTAAGTTICAUDELYK 239
182 HYDONVPLEADEN STORAUSTORALSKORNYRRHWYFLEFFSACHTIGUDELYK 238
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Colorful mitents of green fluorescent protein from Aeguorea
"Colorful mitents of green fluorescent protein from Aeguorea
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0; Gaps
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Meguoreidae, Aequorea.
NCBI_maxib=147615;
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23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nacrodactyla., Submitted (CGT-2001) to the EMBL/GenBank/DDBJ databases. Submitted (CGT-2001) to the EMBL/GenBank/DDBJ databases. EMBL: A4454313. A4133918.1. Interpre: IPR000766; Green_fl_protein. PR001351. GRP. I. Procedn. PR001351. GRP. I. Protein. I. SRDURME. 238 AAI. 25956 MM; 75521EAROCEBA73A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
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01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
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Matches 195; Conservative 20; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Green fluorescent protein.
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Q8WTD0
ID Q8WT
AC Q8WT
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DT 01-M
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122 NRIELKGIDFREDGNILGHKLEYNYNSHNYIMADKOKNGIKVNFKIRHNIEDGSVOLAD 181
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Li S.J., Xia N.S.,
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Luo Wix., Zhang J., Yang H.J., Xie X.Y., Li S.W., Guan B.Q., Chen M.,
Li S.J., Xia N.S.;
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                                                         Eukaryota; Metazoa; Chidaria; Hydrozoa; Hydroida; Leptomedusae;
Anduoraidae; Anduofrea.
NCBI_TRAID-147615;
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Ekkaryota: Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae: Aequorea.
KCBI_TAXID-147615;
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                                                                                                                                                                                                                                                              "Colorful mutants of green fluorescent protein from Aequorea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 64.4%; Score 1075; DB 5; Length 238; Best Local Similarity 91.5%; Pred. No. 5.3e.91. Metches 194; Conservative 20; Mismatches 24; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Colorful mutants of green fluorescent protein from Aequorea
                                                                                                                                                                                                                                                                                                           Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL: AR543427; AR33312.1; -
InterPo: IPR000786; Green_fl_protein.
Pfam. PP01353; GFP: 1.
PrODOM: PD013756; Green_fl_protein; 1.
SROURNCE 238 AA: Z6997 WM; SF800A392173CB84D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     macrodactyla.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases
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Last annotation update)
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01-NAR-2002 (TrEMBLrel. 20, Last seq
01-JUN-2002 (TrEMBLrel. 21, Last ann
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Green fluorescent protein.
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                                               Aequorea macrodactyla.
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                                                                                                                                                                                                                                                                                          macrodactyla.
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VITLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERIIFFKDDGNYKIRAEVKFEGDTLV 121
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                                                                                                           Chen
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Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydrolda; Leptomedusae;
   Aeguorea macrodactyla.
Bukaryota: Metazoa. Cnidaria; Hydrozoa; Hydrolda; Leptomedusae;
Aeguoreldae, Aeguorea.
KOBI_TAXID—147615;
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                                                                                                         Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Guan B.Q.,
Li S.J., Xia min S.;
Li S.J., Xia min S.;
                                                                                                                                                                                                                                                           84.1%; Score 1072; DB 5; Length 238; 81.5%; Pred. No. 9.4e-81;
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                                                                                                                                                                                                                                                                                      24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 maccodactyla.",
Submitted (OCT-201) to the EMBL/GenBank/DDBJ databases.
EMBL, AF43543; AAL33917.1, -.
InterPro; IPR000786; Green_fl_protein.
Proform; PP01375; GFP: 1.
SEOURNCE 238 AA; 27018 MW; 75521EA5534E573A CRC64;
                                                                                                                                               macrodactyla.",
Submitted (GCT-2001) to the EMBL/GenBank/DDBJ databases
EMBL, AF45540; AAL33915.1, -
InterPro; IRPG00786; Green_fl_protein.
Pfan; PF01333; GFP,
ProDom; PD013756; Green_fl_protein;
SEQUENCE 238 AA; 27002 MW; BDSBA2982264C018 CRC64;
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Last annotation update)
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(TrEMBLrel. 21,
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Best Local Similarity 81.59
Matches 194; Conservative
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                                                                                               STRAIN-GFPXM191UV;
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                                                                                                                        VITLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 121
                                                     62 VITLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERIIFFKDDGNYKTRAEVKFEGDTLV 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 VSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL 61
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 VSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTL 61
                     182 HYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHWYLLGFVTAAGITLGMDELYK 239
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Enkaryota: Metazos: Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae: Aequorea.
YESI_EASID—147615;
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Li S.J., Xia N.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Colorful mutants of green fluorescent protein from Aequorea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             macrodactyla.";
Subnitted (OCT-201) to the EMBL/GenBank/DDBJ databases.
EMBL, AR43429, AM13314.1;
InterPro; IRRODO786; Green_fl_protein.
Probom; PDD1373; GFP. 1.
Probom; PDD13756; Green_fl_protein; 1.
SEQUENCE 238 AA; 27047 WW; 5F80A18FA1E7C84D CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                  Green fluorescent protein.
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Best Local Similarity
Matches 194; Conserv
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QBWTC7
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                                        VTTLSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 121
                                                                        122 NRIELKGIDFREDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSSVQLAD 181
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                                                                                                                                            17; Gaps
                                                                                                                                                                                                                                                                                    Cyan fluorescent protein (Fragment).
Montastraea covernosa (great star coral).
Ebkaryota, Metazoa; Cnidaria; Anthozoa; Zoantharia; Scleractinia;
FRAIIna; Pavildae; Montastraea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Green fluorescent protein.

Montastraea cavernosa (greet star coral),
Enkrayota: Metazoa; Conideria; Anthozoa; Zoantharia; Scleractinia;
Favilna; Favildae; Montastraea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 225;
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                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Falkowski P.G., Sun Y.; increscent protein.*;
Montastraen cavernosa fluorescent protein.*;
Submitted (SEP-2020) to the EMBL/GenBank/DDBJ databases.
EMBL; AVOSG460, AALI7905.1;
InterPror; IRMOOV786; Green_fl_protein.
Prob_m; PP001353; GPP; I.
Prob_m; P0013756; Green_fl_protein; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      225 - - 25775 MW; 52DE2F716D083524 CRC64;
                                                                                                                                                                                                                                                            (TrEMBLrcl. 19, Last sequence update) (TrEMBLrcl. 21, Last annotation update)
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01-DEC-2001 (TrEMBLrel, 19, Last seq
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01-JUN-2002 (TrEMBLrel,
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71 CFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGID 130
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Leagar M. Parry T.H., Mazel C., Matz M.V., Lukyanov S.A.,
Falkers H. Carena M. Careboov H. Careboov H.
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